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VisANT

VisANT: Integrative Visual Analysis Tool for Biological Networks and Pathways

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www.openhelix.com

Updated: Q3 2009

OpenHelix

Version 1.0_0809

VisANT Agenda

- Introduction and Credits
- Starting VisANT
- Basic Search and Navigation
- Loading/Saving Data
- Advanced Network Manipulation
- Integration of Data
- Summary
- Exercises

VisANT: http://visant.bu.edu/

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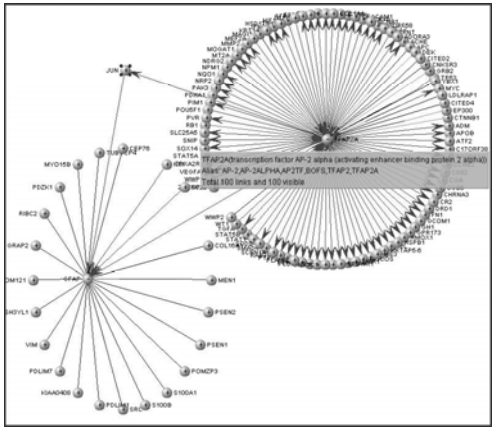
VisANT Introduction

- Biomolecular interaction tool
- Web-based, open-source
- Uses metagraph data structure
- Supports analysis of large networks
- Integrative Data mining

GFAP and TFAP2 Interaction Network



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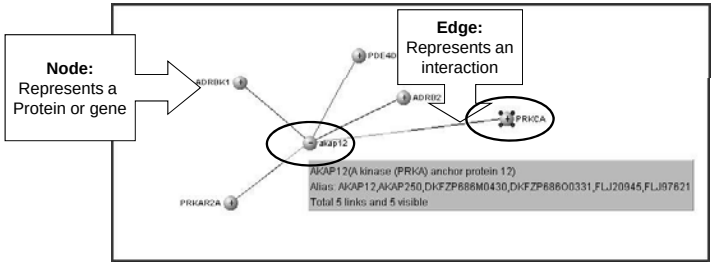
VisANT Data Model



- Data represented as a metagraph with nodes, edges and subnetworks in a nested structure
- Structure allows for one node to have multiple instances and allows a metanode in a metagraph to share nodes

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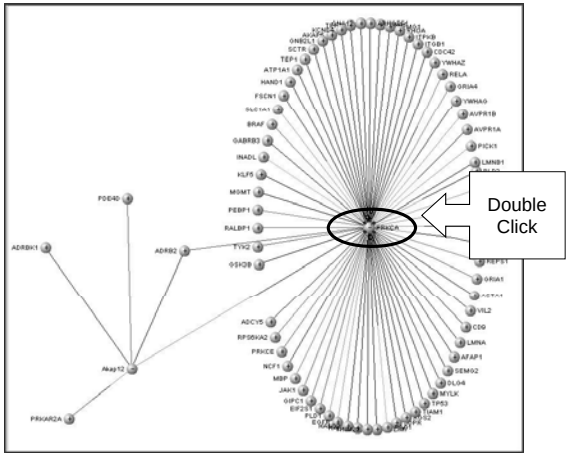
Metanode Expanded



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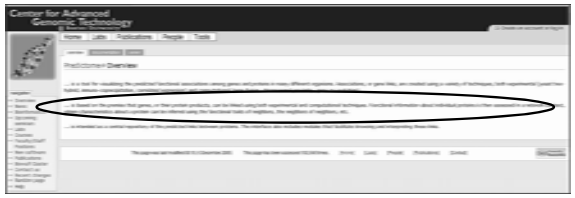
Databases

- **Predictome**: a database of predicted functional associations among genes and proteins http://cagt.bu.edu/page/Predictome



- **BIND, MIPS, HPRD etc.**: provide experimentally determined association data
- **GenBank, SGD, FlyBase, KEGG, GO, HUGO etc.** : provide name normalization and linkout functions

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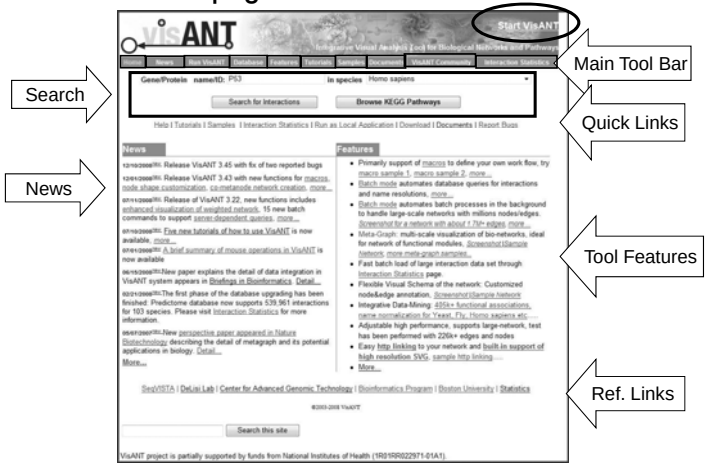
VisANT Homepage



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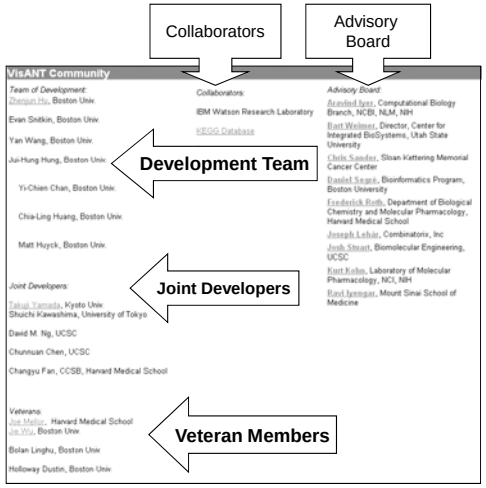
Credits

- Funded partially by grants from the National Institutes of Health (1R01RR022971-01A1)



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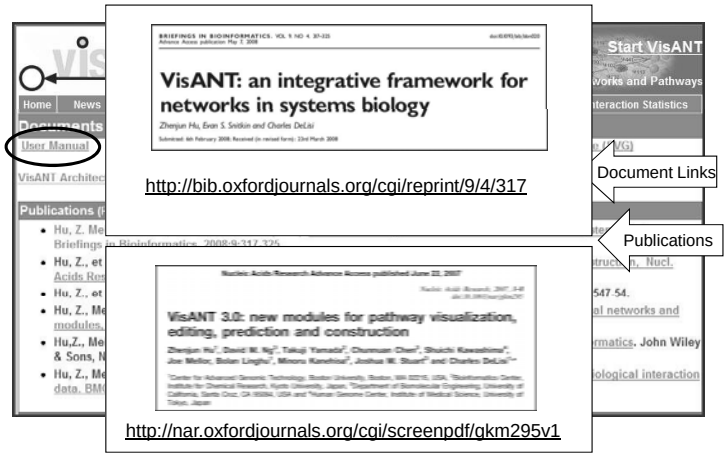
Documents Homepage



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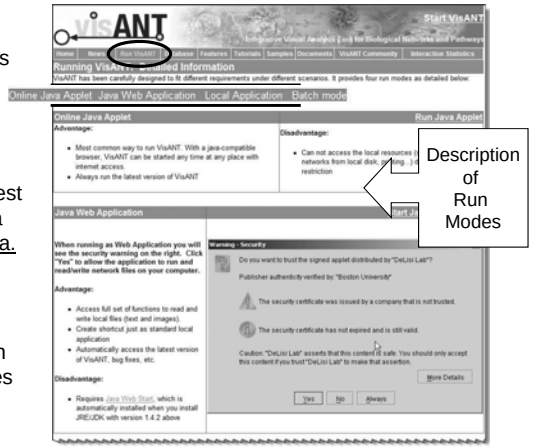
Running VisANT

- Four run modes for VisANT
- All versions require Java: Must install latest version of Java (http://www.java.com/en/)
- Choose run mode based on needed features



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Summary of Run Modes

	Advantages	Disadvantages
■ **Online Java Applet**	Run latest version, easy access with internet	Lack of access to Save/Load and printing features
■ **Java Web Application**	Access to latest version and all features, create shortcut	Requires Java Web start
■ **Local Application**	Access to all features, local copy of VisANT, allows plug-in development, share networks online	Requires manual download of latest software version
■ **Batch Mode**	Automated processing of time consuming tasks and large networks	No user interaction, not all functions available as commands

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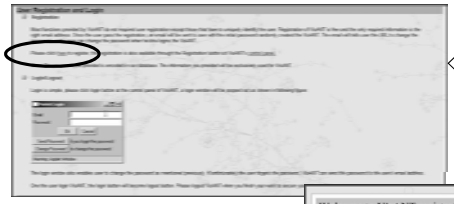
User Registration

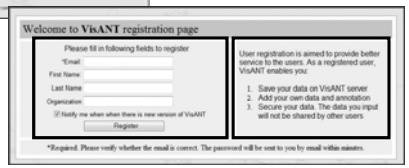
- Documents => user manual

http://visant.bu.edu:8080/test/register.jsp



User Registration Section of User Manual

Registration Page



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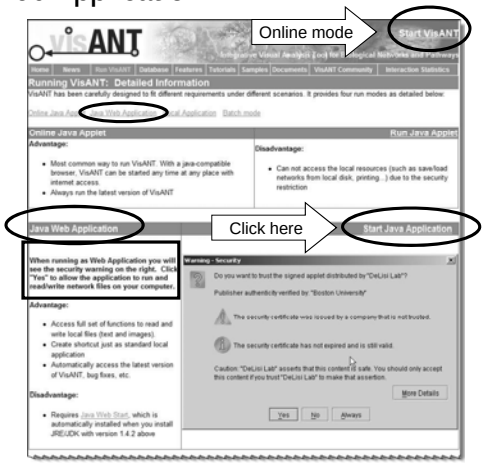
Starting Java Web Application

- Tutorial will use Java Web application mode
- Demonstrate full range of features



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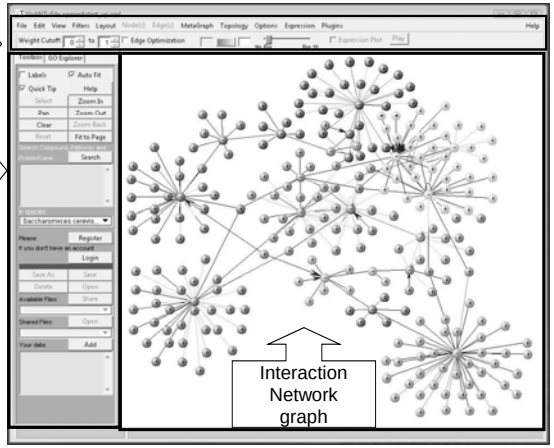
VisANT User Interface

Main Tool Bar

Control Panel



Interaction Network graph

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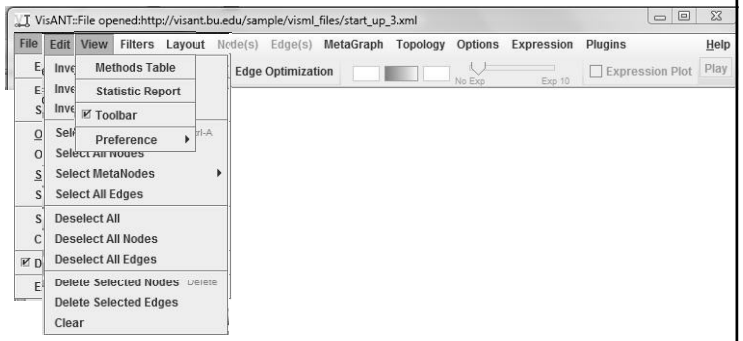
Main Menu Bar: File, Edit & View



- **File**: Export Files, Open, Save, Exit
- **Edit**: Invert node or edge selection, Select, Deselect, Delete
- **View**: methods table, statistics report, Toolbar

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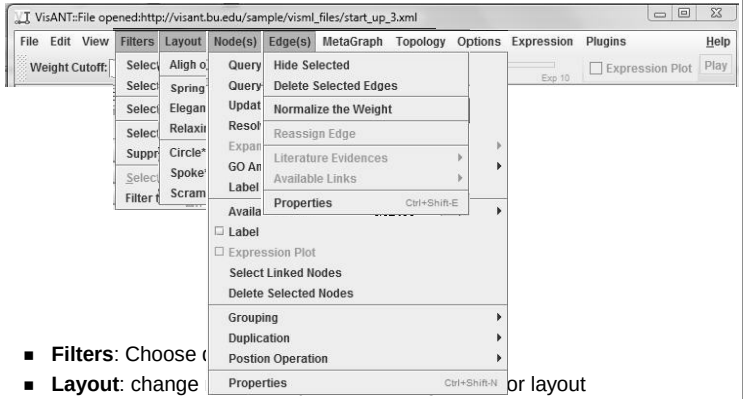
Main Menu Bar: Filters, Layout, Node, Edge



- **Filters**: Choose
- **Layout**: change or layout
- **Node(s)**: when node selected enables functions for node manipulation
- **Edge(s)**: when edge selected enables functions for edge manipulation

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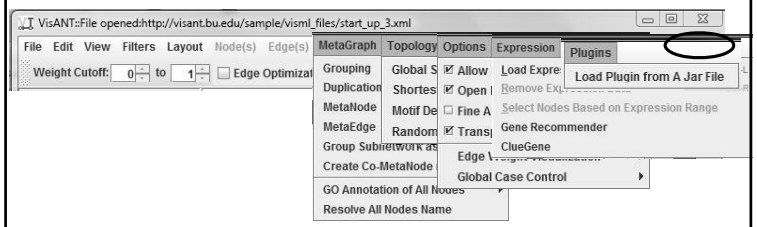
Main Menu Bar, cont.



- **MetaGraph**: meta- nodes and edges, grouping, duplication, manipulation
- **Topology**: graph statistics, shortest path, motif detection
- **Options**: turn on or off pop-up features, visualization features
- **Expression**: loading expression data
- **Plugins**: loading plugins into VisANT
- **Help**: opens up user manual

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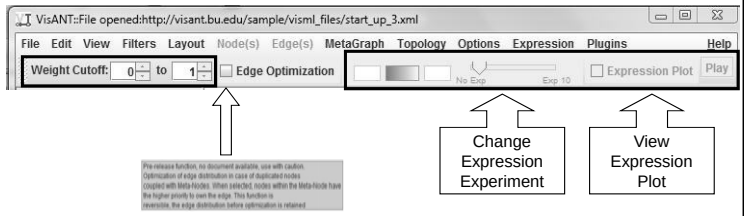
Main Menu Bar, Additional Tools



- **Weight Cutoff –** allows you to choose a range of edge weights from 0 to 1.0 for the edges
- **Edge Optimization-** optimizes the edge distribution. When selected, nodes within the Meta-node have the higher priority to own the edge. Note: Pre-release function, use with caution
- **Expression –** use slider to change expression experiment, and check Expression plot to view an expression plot graph for each node

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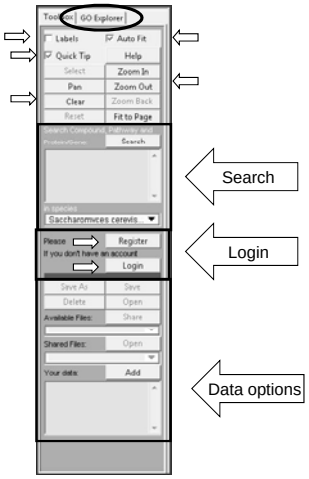
Control Panel

- Labels: turn on/off node labels
- Auto Fit: when checked network will fit to size of panel
- Quick Tip: quickly gain detailed annotation with mouse over
- Zoom In/out and Pane
- Clear graph pane



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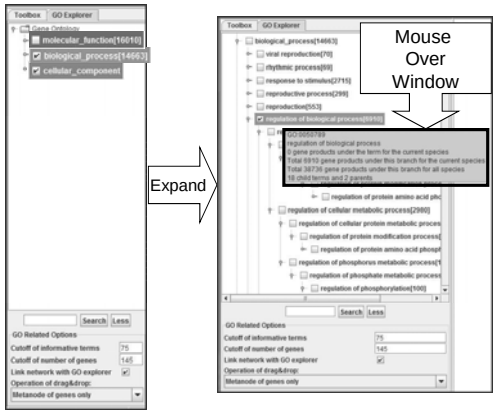
GO Explorer



GO annotation is now available for 13 species:

Saccharomyces cerevisiae,
Arabidopsis thaliana,
Bos taurus,
Caenorhabditis elegans,
Drosophila melanogaster,
Danio rerio,
Gallus gallus,
Homo sapiens,
Magnaporthe grisea,
Mus musculus,
Oryza sativa,
Plasmodium falciparum, and
Rattus norvegicus

- GO annotations will be available as node description if they are available

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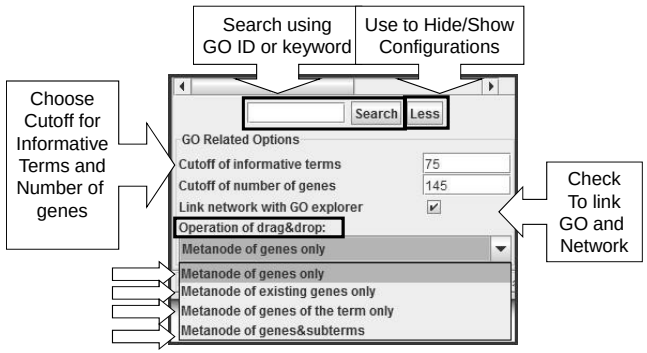
GO Explorer Tools


Search using GO ID or keyword
Use to Hide/Show Configurations
Choose Cutoff for Informative Terms and Number of genes
Check To link GO and Network
Search
Less
GO Related Options
Cutoff of informative terms
75
Cutoff of number of genes
145
Link network with GO explorer
Operation of drag&drop:
Metanode of genes only
Metanode of genes only
Metanode of existing genes only
Metanode of genes of the term only
Metanode of genes&subterms

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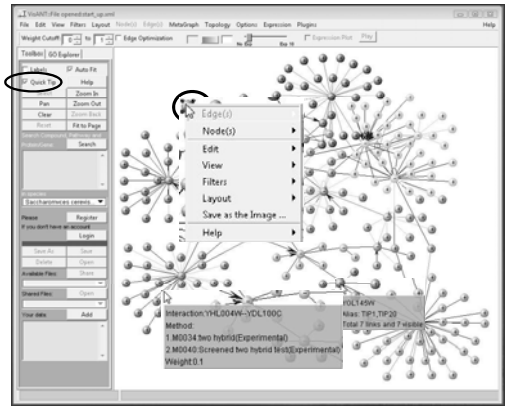
Graph Panel

- Move mouse over node or edge to see label and information
- Click on node to select
- Right click mouse to open pop up menu



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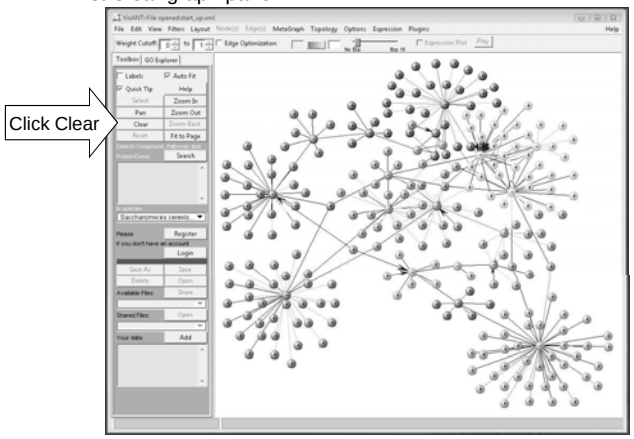
Clear Graph Panel

- First Clear graph pane



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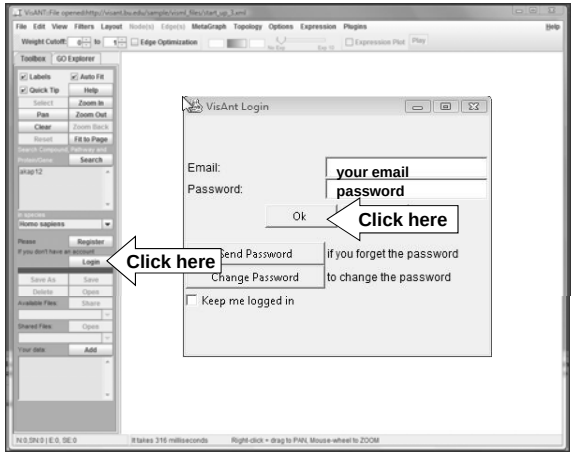
Log In To VisANT



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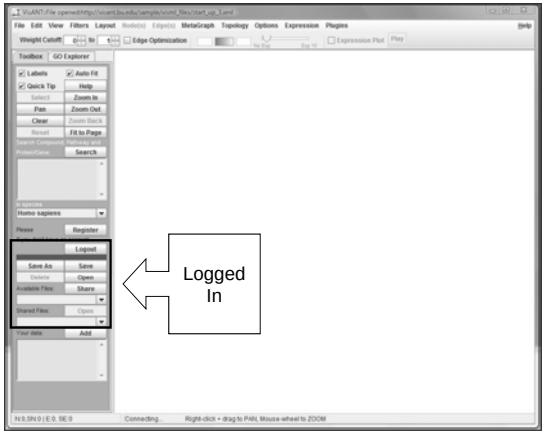
Logged In User Interface



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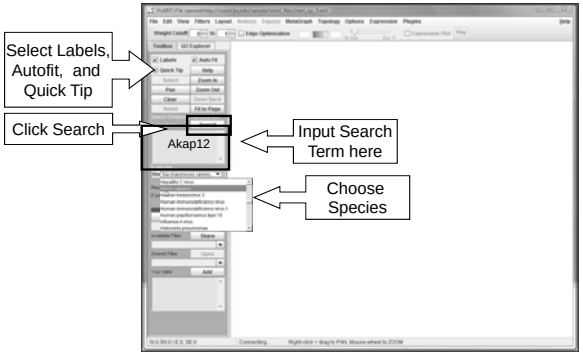
Input Search Term



- Search term: gene, protein can use name/ORF/GI number
- For KEGG pathway search entry must started with "map" followed by KEGG ID
- Multiple entries can be separated by either ',' or space/tab

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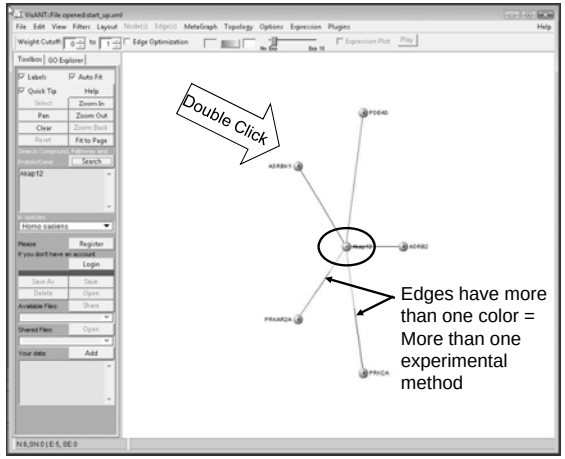
Search Results



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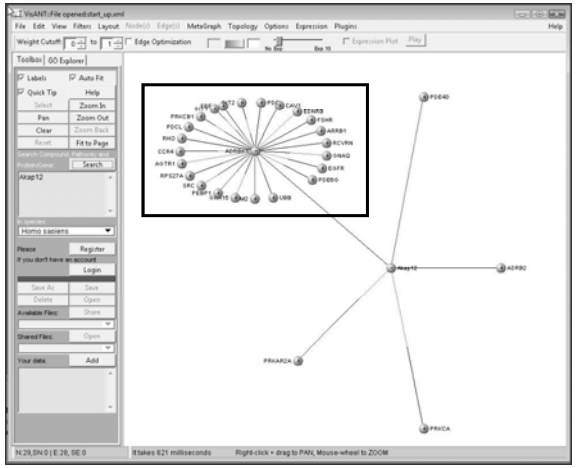
Expand Network



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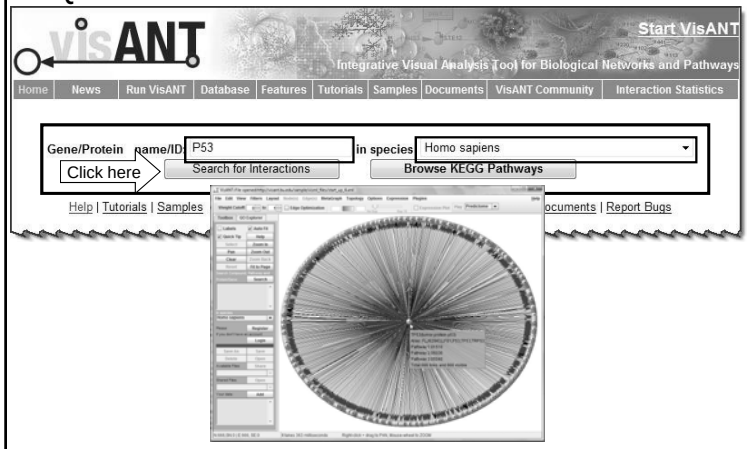
Quick Search



- Opens in online java applet version of VisANT

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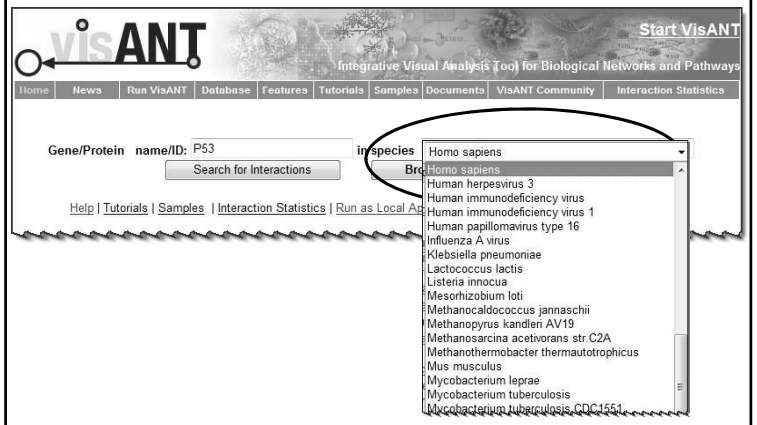
Browse KEGG Pathways



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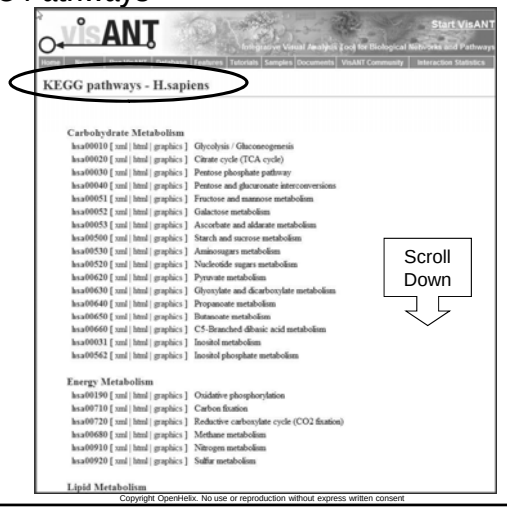
KEGG Pathways


visANT
Start VisANT
KEGG pathways - H.sapiens
Carbohydrate Metabolism
hsa00010 [xml | html | graphics] Glycolysis / Gluconeogenesis
hsa00020 [xml | html | graphics] Citrate cycle (TCA cycle)
hsa00030 [xml | html | graphics] Pentose phosphate pathway
hsa00040 [xml | html | graphics] Pentose and glucuronate interconversions
hsa00051 [xml | html | graphics] Fructose and mannose metabolism
hsa00052 [xml | html | graphics] Galactose metabolism
hsa00053 [xml | html | graphics] Ascorbate and aldarate metabolism
hsa00500 [xml | html | graphics] Starch and sucrose metabolism
hsa00530 [xml | html | graphics] Aminosugars metabolism
hsa00520 [xml | html | graphics] Nucleotide sugars metabolism
hsa00620 [xml | html | graphics] Pyruvate metabolism
hsa00630 [xml | html | graphics] Glyoxylate and dicarboxylate metabolism
hsa00640 [xml | html | graphics] Propanoate metabolism
hsa00650 [xml | html | graphics] Butanoate metabolism
hsa00660 [xml | html | graphics] C5-Branched dibasic acid metabolism
hsa00031 [xml | html | graphics] Inositol metabolism
hsa00562 [xml | html | graphics] Inositol phosphate metabolism
Energy Metabolism
hsa00190 [xml | html | graphics] Oxidative phosphorylation
hsa00710 [xml | html | graphics] Carbon fixation
hsa00720 [xml | html | graphics] Reductive carboxylate cycle (CO2 fixation)
hsa00680 [xml | html | graphics] Methane metabolism
hsa00910 [xml | html | graphics] Nitrogen metabolism
hsa00920 [xml | html | graphics] Sulfur metabolism
Lipid Metabolism
Scroll Down

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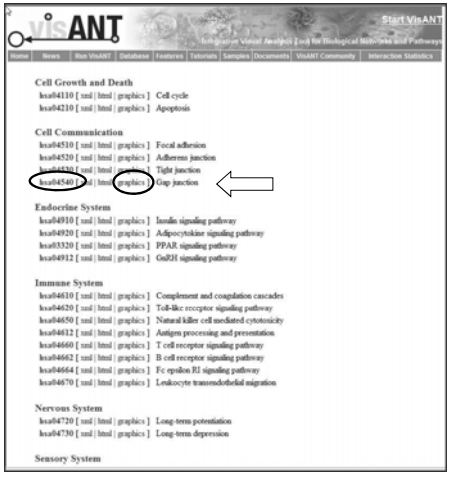
Cell Communication Pathway


visANT
Start VisANT
Cell Growth and Death
hsa04110 [xml | html | graphics] Cell cycle
hsa04210 [xml | html | graphics] Apoptosis
Cell Communication
hsa04510 [xml | html | graphics] Focal adhesion
hsa04520 [xml | html | graphics] Adherens junction
hsa04530 [xml | html | graphics] Tight junction
hsa04540 [xml | html | graphics] Gap junction
Endocrine System
hsa04910 [xml | html | graphics] Insulin signaling pathway
hsa04920 [xml | html | graphics] Adipocytokine signaling pathway
hsa03320 [xml | html | graphics] PPAR signaling pathway
hsa04912 [xml | html | graphics] GnRH signaling pathway
Immune System
hsa04610 [xml | html | graphics] Complement and coagulation cascades
hsa04620 [xml | html | graphics] Toll-like receptor signaling pathway
hsa04650 [xml | html | graphics] Natural killer cell mediated cytotoxicity
hsa04612 [xml | html | graphics] Antigen processing and presentation
hsa04660 [xml | html | graphics] T cell receptor signaling pathway
hsa04662 [xml | html | graphics] B cell receptor signaling pathway
hsa04664 [xml | html | graphics] Fc epsilon RI signaling pathway
hsa04670 [xml | html | graphics] Leukocyte transendothelial migration
Nervous System
hsa04720 [xml | html | graphics] Long-term potentiation
hsa04730 [xml | html | graphics] Long-term depression
Sensory System

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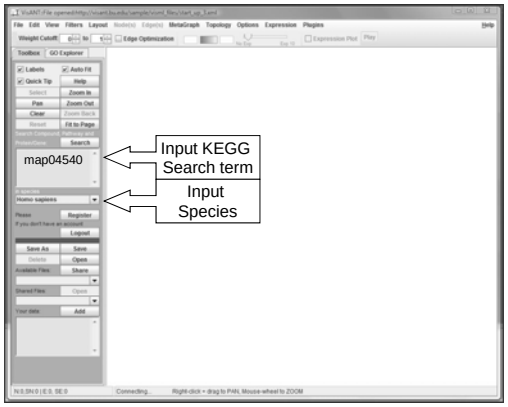
Search KEGG Pathway



- Search term “map” and KEGG ID number
- Species must match

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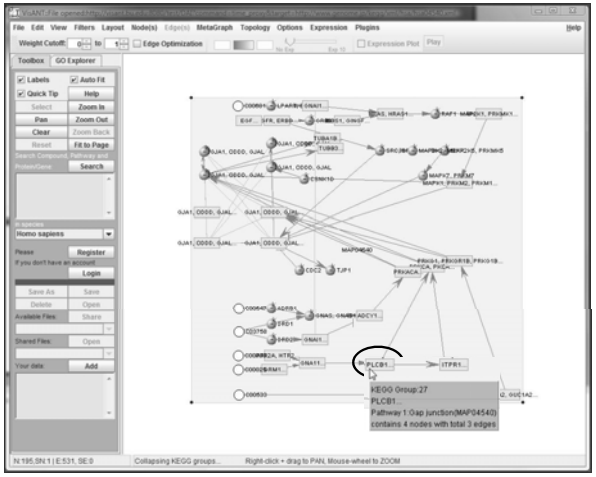
KEGG Gap Junction Pathway



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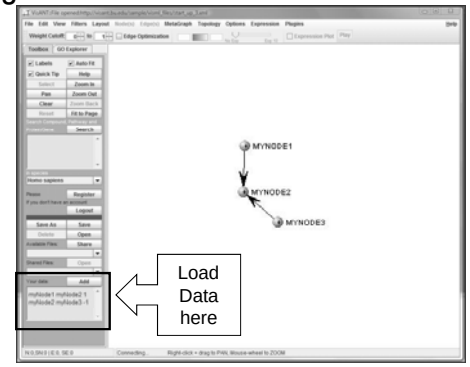
Loading Data



- **Function is only available after users login**
- **Data format**:

Column 1	Column 2	Column3	Column4
Starting node	Ending node	Direction	Method

- **Only Column 1 required**

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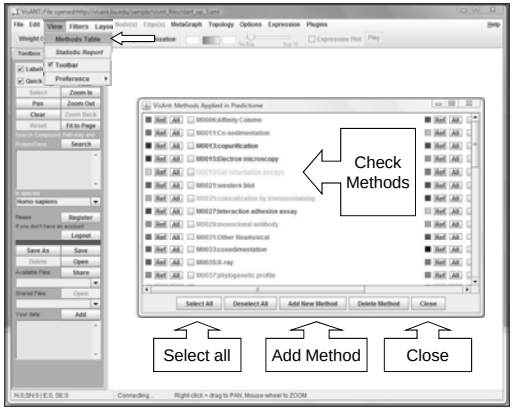
Method Based Data Loading

- For large scale analysis of interactions based on method



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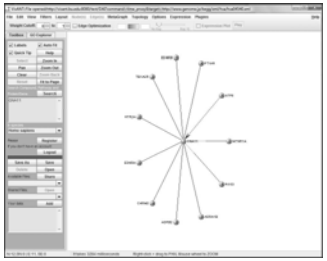
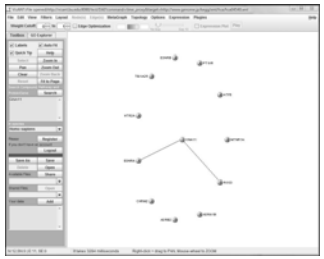
Use of Methods Table



GNA11
With all
Methods
Selected

GNA11
With only
Two-hybrid
Selected



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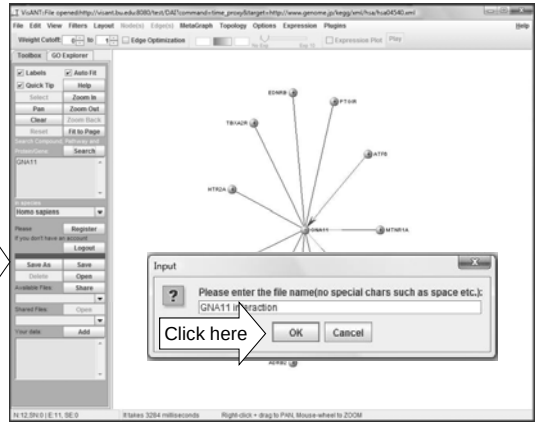
Saving Data



- Must be logged in as a registered user

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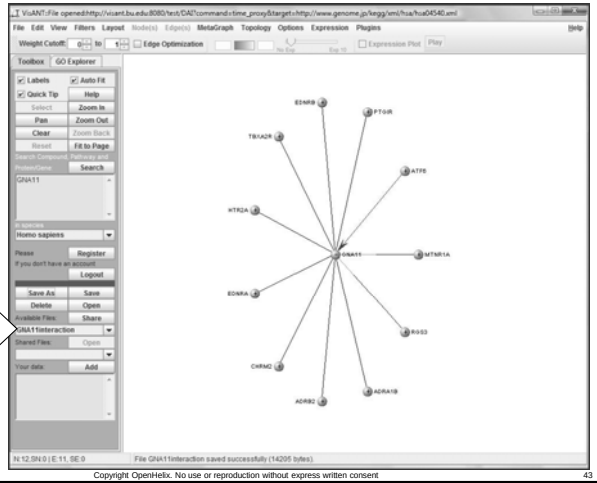
Available Files

File
Now
Available



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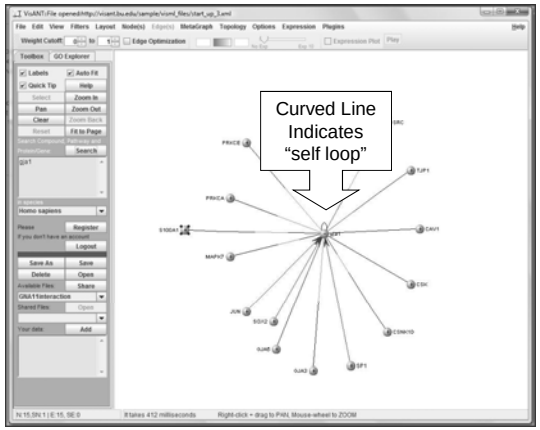
Advanced Techniques



- A connection to the node itself is called a "self loop"

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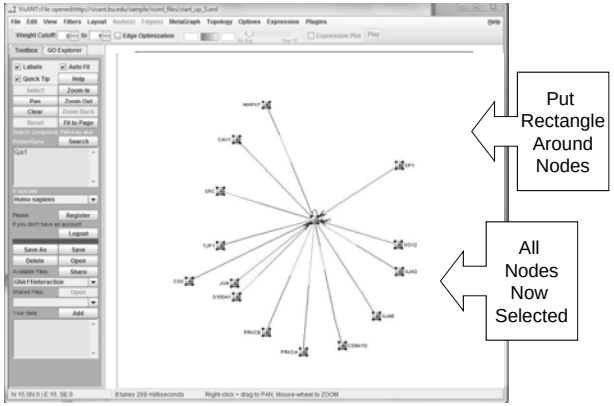
Select Multiple Nodes



- Once selected, click and drag on node or edge to move as a group

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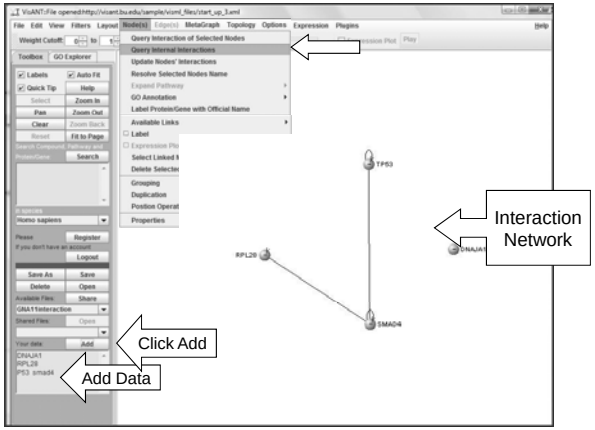
Find Connections



- Find connections between a set of proteins

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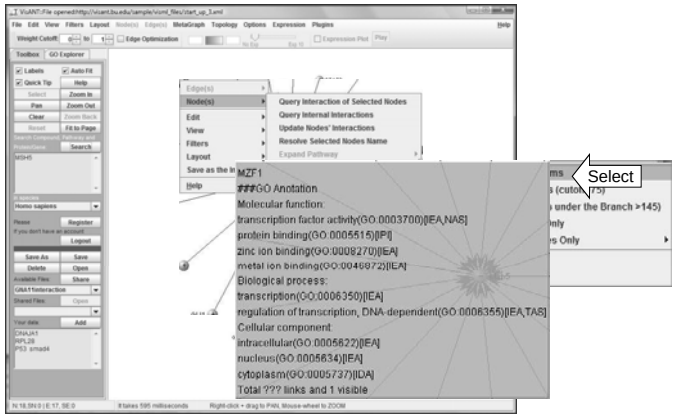
Add GO Annotation



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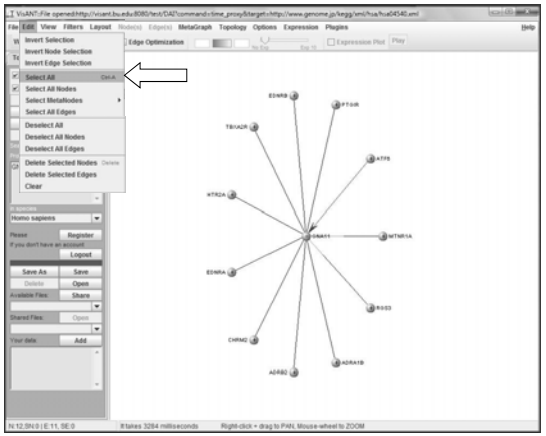
Integration of Interactome



- Find only those interactions with multiple methods

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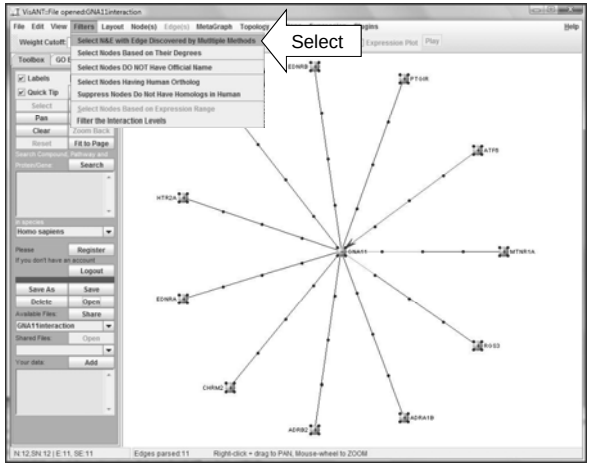
Filter by Multiple Methods



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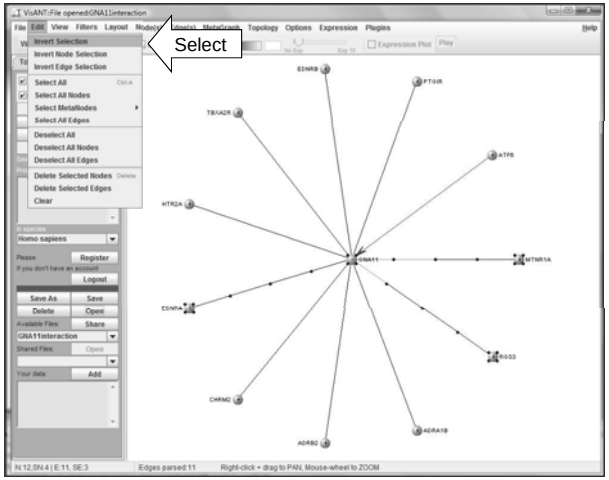
Invert Selection



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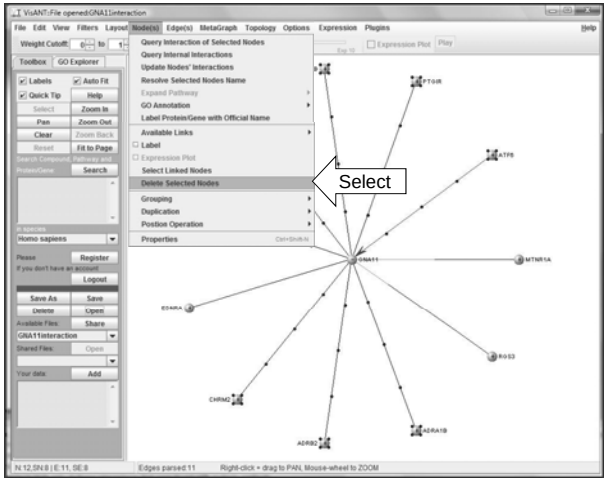
Delete Selected Nodes



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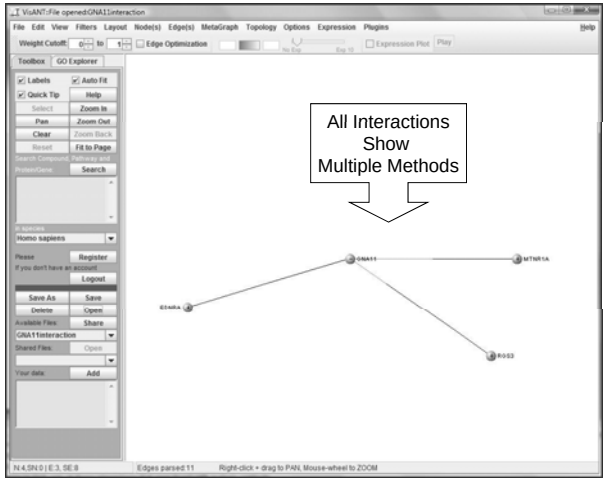
Interactions with Multiple Methods



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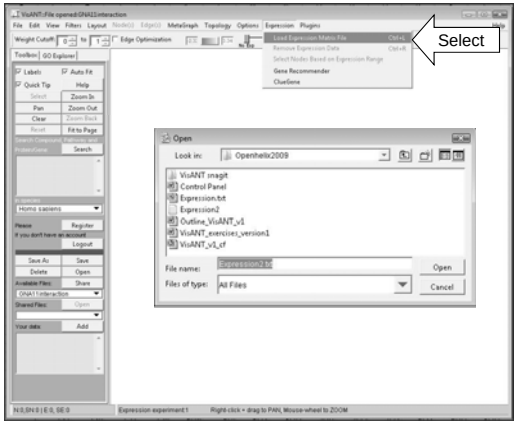
Integration of Expression Profile



- Expression menu can only be run with Java Web start version or Local Application

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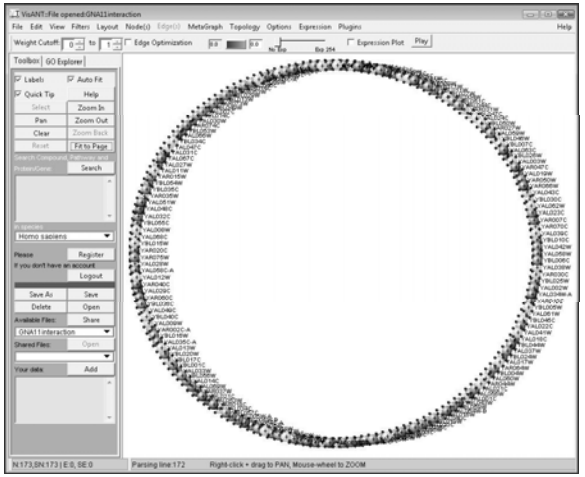
Loaded Expression Data



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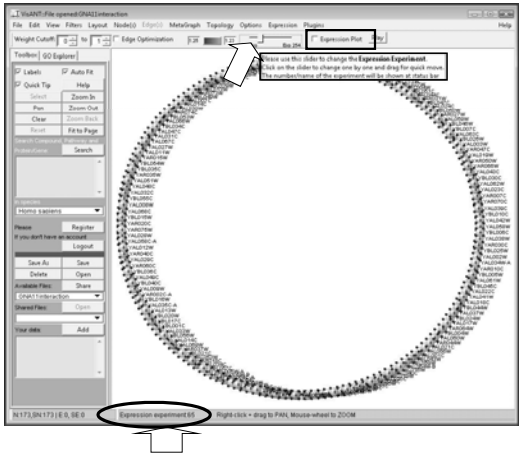
Change Expression Experiment



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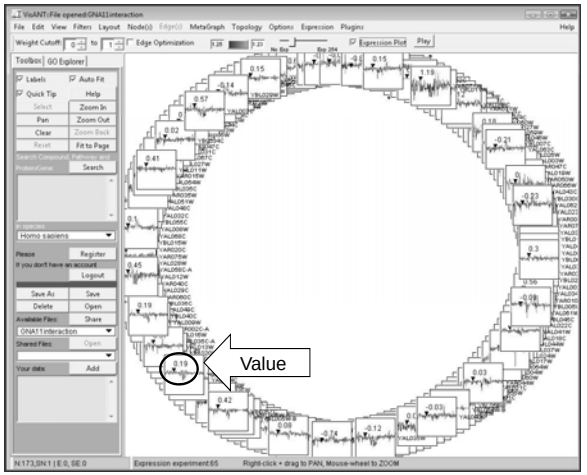
Expression Plot



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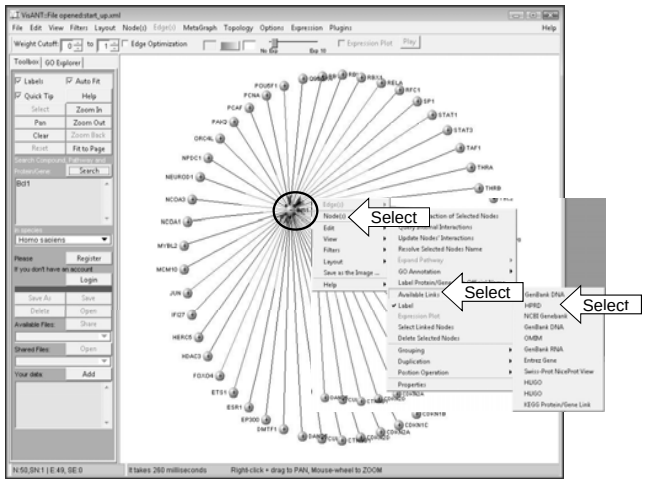
Integration with Other Annotation



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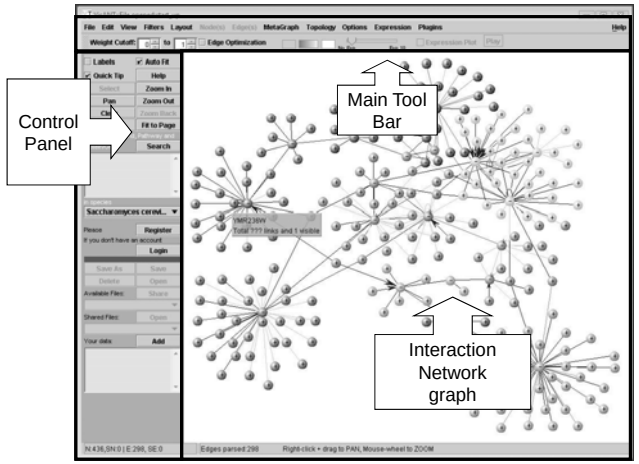

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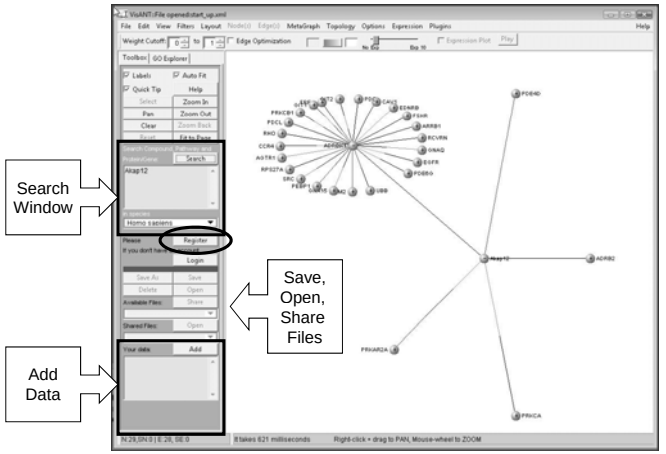
Search for Interactions



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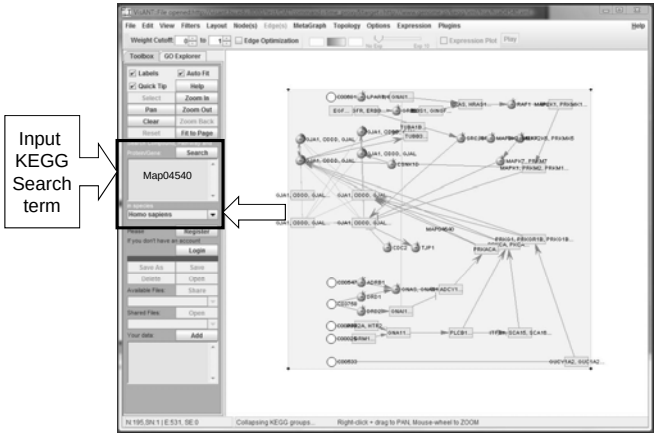
Search for KEGG Pathways



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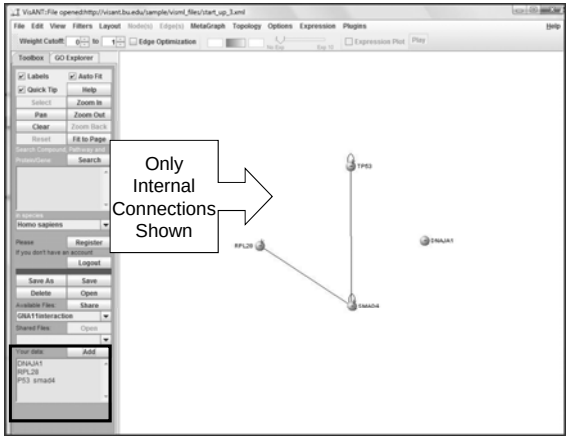
Find Connections



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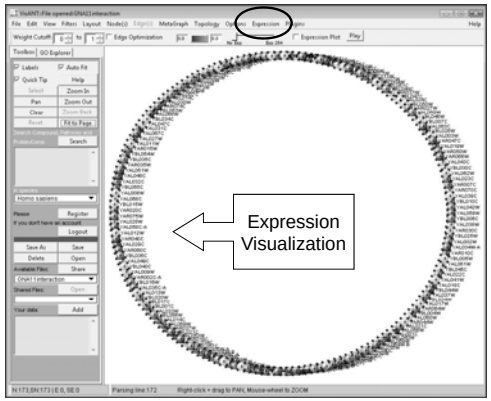
Data Integration

- Integrate data on GO annotations
- Link to GenBank, OMIM, Entrez Gene, HUGO, and KEGG
- Integrate Expression data



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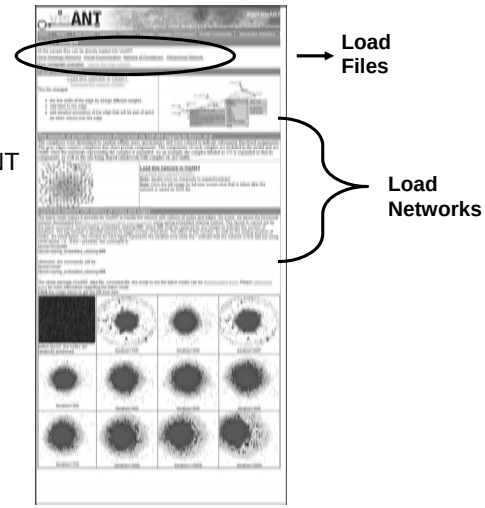
Sample Files

- Load these files directly into VisANT



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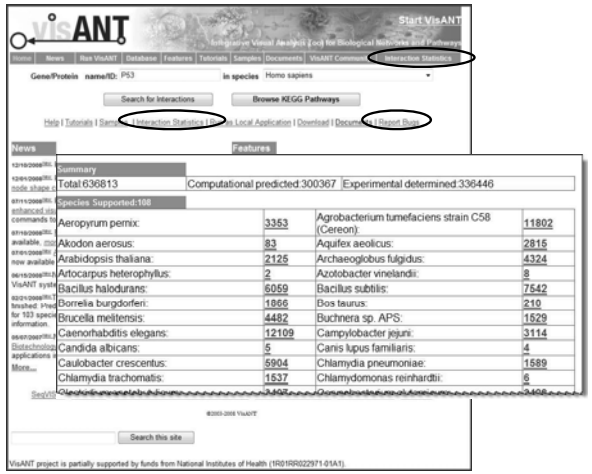
VisANT Summary



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